

<110> Jager, Dirk  
Scanlan, Matthew  
Gure, Ali  
Jager, Elke  
Knuth, Alexander  
Old, Lloyd  
Chen, Yao-tseng

<120> Isolated Nucleic Acid Molecules Encoding Cancer Associated Antigens,  
the Antigens per se, and Uses Thereof

<130> LUD 5615

<140> 09/451,739

<141> 1999-11-30

<160> 19

<210> 1  
<211> 1533  
<212> DNA  
<213> Homo sapiens  
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<221> CDS  
<222> 235  
<223> unknown  
<400> 1

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<210> 2

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&lt;211&gt; 1143

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2

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cccgcggggg	ctcggagaca	gtttcaggcc	gcattcttgc	tgacccgagg	gtggggccgc	180
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agccaggagc	tgggcgacga	gaagatccag	atcgtgagcc	aqatggtgga	gctggtggag	360
aaccgcacgc	ggcaggtgga	cagccacgtg	gagctgttcg	aqccgcagca	ggagctgggc	420
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aca						1143

&lt;210&gt; 3

&lt;211&gt; 742

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;400&gt; 3

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ggcaacagcg	gcaaggttgg	ggcgacaggg	cccaaggcgg	aggcggcagc	gcaggctgac	420
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tccaagaaga	agaagcgtc	caaggccacg	gcggagcgag	aggcgtcccc	tgccgacctc	600
ccatcgacc	ccacgaacc	ccctactgt	ctglgcaacc	aggtctacta	tggggagatg	660
atcggtcg	acaacgacga	gtgcacctc	gagtggttcc	acttctcgtg	cgtggggctc	720
aatcataaac	ccaaggcca	gt				742

&lt;210&gt; 4

&lt;211&gt; 857

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 4

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ctttgtctcc	aagcggttcc	aaactgagta	ccgggagacg	acacaaagg	agggcggtga	180
cggatggcgc	agggcgggga	gcgccttagg	ctgctgggag	tgttggctcg	qccgcggaat	240
ggagatcctg	aaggagctag	acgagtctca	cqagcgttc	agtcgggaga	cagacggggc	300

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gcagaagcgg cggatgctgc actgtgtgca ggcgcgcgtg atccgcagcc aggagctggg 360
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ggtggacagc cactgggagc tgttcgagcc gcagcaggag ctgggcgaca cagcggggcaa 480
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&lt;210&gt; 5

&lt;211&gt; 279

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 5

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1                               10               15
Glu Asp Tyr Leu Asp Ser Ile Glu Ser Leu Pro Phe Asp Leu Gln Arg
20               25               30
Asn Val Ser Leu Met Arg Glu Ile Asp Ala Lys Tyr Gln Glu Ile Leu
35               40               45
Lys Glu Leu Asp Glu Cys Tyr Glu Arg Phe Ser Arg Glu Thr Asp Gly
50               55               60
Ala Gln Lys Arg Arg Met Leu His Cys Val Gln Arg Ala Leu Ile Arg
65               70               75               80
Ser Gln Glu Leu Gly Asp Glu Lys Ile Gln Ile Val Ser Gln Met Val
85               90               95
Glu Leu Val Glu Asn Arg Thr Arg Gln Val Asp Ser His Val Glu Leu
100              105              110
Phe Glu Ala Gln Gln Glu Leu Gly Asp Thr Val Gly Asn Ser Gly Lys
115              120              125
Val Gly Ala Asp Arg Pro Asn Gly Asp Ala Val Ala Gln Ser Asp Lys
130              135              140
Pro Asn Ser Lys Arg Ser Arg Arg Gln Arg Asn Asn Glu Asn Arg Glu
145              150              155              160
Asn Ala Ser Ser Asn His Asp His Asp Asp Gly Ala Ser Gly Thr Pro
165              170              175
Lys Glu Lys Lys Ala Lys Thr Ser Lys Lys Lys Lys Arg Ser Lys Ala
180              185              190
Lys Ala Glu Arg Glu Ala Ser Pro Ala Asp Leu Pro Ile Asp Pro Asn
195              200              205
Glu Pro Thr Tyr Cys Leu Cys Asn Gln Val Ser Tyr Gly Glu Met Ile
210              215              220
Gly Cys Asp Asn Asp Glu Cys Pro Ile Glu Trp Phe His Phe Ser Cys
225              230              235              240
Val Gly Leu Asn His Lys Pro Lys Gly Lys Trp Tyr Cys Pro Lys Cys
245              250              255
Arg Gly Glu Asn Glu Lys Thr Met Asp Lys Ala Leu Glu Lys Ser Lys
260              265              270
Lys Glu Arg Ala Tyr Asn Arg
275

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&lt;210&gt; 6

&lt;211&gt; 210

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&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;400&gt; 6

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Met Leu His Cys Val Gln Arg Ala Leu Ile Arg Ser Gln Glu Leu Gly
1      5      10      15
Asp Glu Lys Ile Gln Ile Val Ser Gln Met Val Glu Leu Val Glu Asn
20      25      30
Arg Thr Arg Gln Val Asp Ser His Val Glu Leu Phe Glu Ala Gln Gln
35      40      45
Glu Leu Gly Asp Thr Val Gly Asn Ser Gly Lys Val Gly Ala Asp Arg
50      55      60
Pro Asn Gly Asp Ala Val Ala Gln Ser Asp Lys Pro Asn Ser Lys Arg
65      70      75      80
Ser Arg Arg Gln Arg Asn Asn Glu Asn Arg Glu Asn Ala Ser Ser Asn
85      90      95
His Asp His Asp Asp Gly Ala Ser Gly Thr Pro Lys Glu Lys Lys Ala
100     105     110
Lys Thr Ser Lys Lys Lys Lys Arg Ser Lys Ala Lys Ala Glu Arg Glu
115     120     125
Ala Ser Pro Ala Asp Leu Pro Ile Asp Pro Asn Glu Pro Thr Tyr Cys
130     135     140
Leu Cys Asn Gln Val Ser Tyr Gly Glu Met Ile Gly Cys Asp Asn Asp
145     150     155     160
Glu Cys Pro Ile Glu Trp Phe His Phe Ser Cys Val Gly Leu Asn His
165     170     175
Lys Pro Lys Gly Lys Trp Tyr Cys Pro Lys Cys Arg Gly Glu Asn Glu
180     185     190
Lys Thr Met Asp Lys Ala Leu Glu Lys Ser Lys Lys Glu Arg Ala Tyr
195     200     205
Asn Arg
210

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&lt;210&gt; 7

&lt;211&gt; 235

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 7

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Met Glu Ile Leu Lys Glu Leu Asp Glu Cys Tyr Glu Arg Phe Ser Arg
1      5      10      15
Glu Thr Asp Gly Ala Gln Lys Arg Arg Met Leu His Cys Val Gln Arg
20      25      30
Ala Leu Ile Arg Ser Gln Glu Leu Gly Asp Glu Lys Ile Gln Ile Val
35      40      45
Ser Gln Met Val Glu Leu Val Glu Asn Arg Thr Arg Gln Val Asp Ser
50      55      60
His Val Glu Leu Phe Glu Ala Gln Gln Glu Leu Gly Asp Thr Val Gly
65      70      75      80
Asn Ser Gly Lys Val Gly Ala Asp Arg Pro Asn Gly Asp Ala Val Ala
85      90      95
Gln Ser Asp Lys Pro Asn Ser Lys Arg Ser Arg Arg Gln Arg Asn Asn
100     105     110
Glu Asn Arg Glu Asn Ala Ser Ser Asn His Asp His Asp Asp Gly Ala
115     120     125
Ser Gly Thr Pro Lys Glu Lys Lys Ala Lys Thr Ser Lys Lys Lys Lys
130     135     140

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Arg Ser Lys Ala Lys Ala Glu Arg Glu Ala Ser Pro Ala Asp Leu Pro  
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 Ile Asp Pro Asn Glu Pro Thr Tyr Cys Leu Cys Asn Gln Val Ser Tyr  
 165 170 175  
 Gly Glu Met Ile Gly Cys Asp Asn Asp Glu Cys Pro Ile Glu Trp Phe  
 180 185 190  
 His Phe Ser Cys Val Gly Leu Asn His Lys Pro Lys Gly Lys Trp Tyr  
 195 200 205  
 Cys Pro Lys Cys Arg Gly Glu Asn Glu Lys Thr Met Asp Lys Ala Leu  
 210 215 220  
 Glu Lys Ser Lys Lys Glu Arg Ala Tyr Asn Arg  
 225 230 235

<210> 8  
 <211> 772  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> CDS  
 <222> 689,714  
 <223> unknown nucleotides at positions 689 and 714  
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 agcagggctc catggccaag gcttagcggc aggcgtcccc cgcagacctc cccatcgacc 180  
 ccagcagacc cctctactgq gagatgatcc gctgcgacca cgaatgcccc atcgagtggg 240  
 tccgcttctc gtgtgtgagt ctcaaccata aaccaaaagc caagtggtag tgttccagat 300  
 gccggggaaa gaacgatggg caaagccctt gagaagtcca gaaaaaaac agggcttata 360  
 acaggtagtt tggggacatg cgtclaatag tgaggagaac aaaataagcc agtgtgttga 420  
 ttaacattgcc acctttgctg aggtgcagga agtgtaaaat qtatahtttt aaagaatgtt 480  
 gtttagagcc gggcggggtg gctcaacgct gtaatcccag cactttggga ggccgagggg 540  
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 attcgggagg ctgaggcagg agaattggnt gaacctggga ggtggagctt gcantgagcc 720  
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<210> 9  
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32

<210> 10  
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23

<210> 11  
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 <212> DNA

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21

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23

<210> 13  
 <211> 23  
 <212> DNA  
 <213> Homo sapiens  
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23

<210> 14  
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 <212> DNA  
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 <400> 14  
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23

<210> 15  
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 <212> DNA  
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 aqaatgaaca aacattgaga gcagatgaga tactcccatc aqaatccaaa caaaaggact 240  
 atgaagaaaq ttcttgggat tctgagagtc tctgtgagac tgtttcacag aaggatgtgt 300  
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 ctctgataa agatggtttt ctgaaggctc cctgcagaat gaaagtttct attccaacta 420  
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 atgaacaaac attgagagca gatcagatgt tcccttcaga atcaaaacaa aagaaggttg 600  
 aagaataatc ttgggattct gagagctctc gtgagactgt ttacacagaag gatgtgtgtg 660  
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 aatgggaaca agagctctgc agtgtcagat tgactttaaa ccaagaagaa gagaagagaa 960  
 gaaatgccga tatattaat gaaaaaatte gggagaatt aggaagaatc gaagagcagc 1020  
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ccatttataa aaccctgata ttccaatatg gaaaaaaaaa anaaaaaaa 2030

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&lt;210&gt; 16

&lt;211&gt; 512

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 16

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Met Lys Val Ser Ile Pro Thr Lys Ala Leu Glu Leu Met Asp Met Gln
1          5          10          15
Thr Phe Lys Ala Glu Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro Ala
20          25          30
Ile Glu Met Gln Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys Asn
35          40          45
Glu Gln Thr Leu Arg Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys Gln
50          55          60
Lys Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr
65          70          75          80
Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Thr His Gln Lys Glu
85          90          95
Ile Asp Lys Ile Asn Gly Lys Leu Glu Glu Ser Pro Asp Asn Asp Gly
100         105         110
Phe Leu Lys Ala Pro Cys Arg Met Lys Val Ser Ile Pro Thr Lys Ala
115         120         125
Leu Glu Leu Met Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Glu Lys
130         135         140
Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Gln Lys Ser Val Pro Asn
145         150         155         160
Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Gln Met
165         170         175
Phe Pro Ser Glu Ser Lys Gln Lys Lys Val Glu Glu Asn Ser Trp Asp
180         185         190
Ser Glu Ser Leu Arg Glu Thr Val Ser Gln Lys Asp Val Cys Val Pro
195         200         205
Lys Ala Thr His Gln Lys Glu Met Asp Lys Ile Ser Gly Lys Leu Glu
210         215         220
Asp Ser Thr Ser Leu Ser Lys Ile Leu Asp Thr Val His Ser Cys Glu
225         230         235         240
Arg Ala Arg Glu Leu Gln Lys Asp His Cys Glu Gln Arg Thr Gly Lys
245         250         255
Met Glu Gln Met Lys Lys Lys Phe Cys Val Leu Lys Lys Lys Leu Ser
260         265         270

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Glu Ala Lys Glu Ile Lys Ser Gln Leu Glu Asn Gln Lys Val Lys Trp  
 275 280 285  
 Glu Gln Glu Leu Cys Ser Val Arg Leu Thr Leu Asn Gln Glu Glu Glu  
 290 295 300  
 Lys Arg Arg Asn Ala Asp Ile Leu Asn Glu Lys Ile Arg Glu Glu Leu  
 305 310 315 320  
 Gly Arg Ile Glu Glu Gln His Arg Lys Glu Leu Glu Val Lys Gln Gln  
 325 330 335  
 Leu Glu Gln Ala Leu Arg Ile Gln Asp Ile Glu Leu Lys Ser Val Glu  
 340 345 350  
 Ser Asn Leu Asn Gln Val Ser His Thr His Glu Asn Glu Asn Tyr Leu  
 355 360 365  
 Leu His Glu Asn Cys Met Leu Lys Lys Glu Ile Ala Met Leu Lys Leu  
 370 375 380  
 Glu Ile Ala Thr Leu Lys His Gln Tyr Gln Glu Lys Glu Asn Lys Tyr  
 385 390 395 400  
 Phe Glu Asp Ile Lys Ile Leu Lys Glu Lys Asn Ala Glu Leu Gln Met  
 405 410 415  
 Thr Leu Lys Leu Lys Glu Glu Ser Leu Thr Lys Arg Ala Ser Gln Tyr  
 420 425 430  
 Ser Gly Gln Leu Lys Val Leu Ile Ala Glu Asn Thr Met Leu Thr Ser  
 435 440 445  
 Lys Leu Lys Glu Lys Gln Asp Lys Glu Ile Leu Glu Ala Glu Ile Glu  
 450 455 460  
 Ser His His Pro Arg Leu Ala Ser Ala Val Gln Asp His Asp Gln Ile  
 465 470 475 480  
 Val Thr Ser Arg Lys Ser Gln Glu Pro Ala Phe His Ile Ala Gly Asp  
 485 490 495  
 Ala Cys Leu Gln Arg Lys Met Asn Val Asp Val Ser Ser Thr Asp Ile  
 500 505 510

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 cacacaaagc ttctaggatt tggcacagcc agag 34

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 <211> 294  
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 1 5 10 15  
 Asp Pro Gly Pro Val Ala Arg Gly Arg Gly Cys Ser Ser Asp Arg Leu  
 20 25 30



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Pro Arg Pro Ala Gly Pro Ala Arg Arg Gln Phe Gln Ala Ala Ser Leu
    35          40          45
Leu Thr Arg Gly Trp Gly Arg Ala Trp Pro Trp Lys Gln Ile Leu Lys
    50          55          60
Glu Leu Asp Glu Cys Tyr Glu Arg Phe Ser Arg Glu Thr Asp Gly Ala
    65          70          75          80
Gln Lys Arg Arg Met Leu His Cys Val Gln Arg Ala Leu Ile Arg Ser
    85          90          95
Gln Glu Leu Gly Asp Glu Lys Ile Gln Ile Val Ser Gln Met Val Glu
    100          105          110
Leu Val Glu Asn Arg Thr Arg Gln Val Asp Ser His Val Glu Leu Phe
    115          120          125
Glu Ala Gln Gln Glu Leu Gly Asp Thr Val Gly Asn Ser Gly Lys Val
    130          135          140
Gly Ala Asp Arg Pro Asn Gly Asp Ala Val Ala Gln Ser Asp Lys Pro
    145          150          155          160
Asn Ser Lys Arg Ser Arg Arg Gln Arg Asn Asn Glu Asn Arg Glu Asn
    165          170          175
Ala Ser Ser Asn His Asp His Asp Asp Gly Ala Ser Gly Thr Pro Lys
    180          185          190
Glu Lys Lys Ala Lys Thr Ser Lys Lys Lys Arg Ser Lys Ala Lys
    195          200          205
Ala Glu Arg Glu Ala Ser Pro Ala Asp Leu Pro Ile Asp Pro Asn Glu
    210          215          220
Pro Thr Tyr Cys Leu Cys Asn Gln Val Ser Tyr Gly Glu Met Ile Gly
    225          230          235          240
Cys Asp Asn Asp Glu Cys Pro Ile Glu Trp Phe His Phe Ser Cys Val
    245          250          255
Gly Leu Asn His Lys Pro Lys Gly Lys Trp Tyr Cys Pro Lys Cys Arg
    260          265          270
Gly Glu Asn Glu Lys Thr Met Asp Lys Ala Leu Glu Lys Ser Lys Lys
    275          280          285
Glu Arg Ala Tyr Asn Arg
    290

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